ALIGNMENTS

RESULT 1
US-10-479-446-2
; Sequence 2, Application US/10479446
; Publication No. US20050112749A1
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Schulein, Martin
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Gibson, Keith
; TITLE OF INVENTION: Endo-beta-1,4-glucanases
; FILE REFERENCE: 10184.204-US
; CURRENT APPLICATION NUMBER: US/10/479,446
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-479-446-2

Query Match 100.0%; Score 4131; DB 5; Length 773;
Best Local Similarity 100.0%; Pred. No. 3.5e-298;
Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    1 AEGNTREDNFKHLLGNDNVKRPSEAGALQLQEVDGQMTLVDQHGEKIQLRGMSTHGLQWF 60

Qy   61 PEILNDNAYKALANDWESNMIRLAMYVGENGYASNPELIKSRVIKGIDLAIENDMYVIVD 120
Db   61 PEILNDNAYKALANDWESNMIRLAMYVGENGYASNPELIKSRVIKGIDLAIENDMYVIVD 120

Qy  121 WHVHAPGDPRDPVYAGAEDFFRDIAALYPNNPHIIYELANEPSSNNNGGAGIPNNEEGWN 180
Db  121 WHVHAPGDPRDPVYAGAEDFFRDIAALYPNNPHIIYELANEPSSNNNGGAGIPNNEEGWN 180

Qy  181 AVKEYADPIVEMLRDSGNADDNIIIVGSPNWSQRPDLAADNPINDHHTMYTVHFYTGSHA 240
Db  181 AVKEYADPIVEMLRDSGNADDNIIIVGSPNWSQRPDLAADNPINDHHTMYTVHFYTGSHA 240

Qy  241 ASTESYPPETPNSERGNVMSNTRYALENGVAVFATEWGTSQANGDGGPYFDEADVWIEFL 300
Db  241 ASTESYPPETPNSERGNVMSNTRYALENGVAVFATEWGTSQANGDGGPYFDEADVWIEFL 300

Qy  301 NENNISWANWSLTNKNEVSGAFTPFELGKSNATNLDPGPDHVWAPEELSLSGEYVRARIK 360
Db  301 NENNISWANWSLTNKNEVSGAFTPFELGKSNATNLDPGPDHVWAPEELSLSGEYVRARIK 360

Qy  361 GVNYEPIDRTKYTKVLWDFNDGTKQGFGVNSDSPNKELIAVDNENNTLKVSGLDVSNDVS 420
Db  361 GVNYEPIDRTKYTKVLWDFNDGTKQGFGVNSDSPNKELIAVDNENNTLKVSGLDVSNDVS 420

Qy  421 DGNFWANARLSADGWGKSVDILGAEKLTMDVIVDEPTTVAIAAIPQSSKSGWANPERAVR 480
Db  421 DGNFWANARLSADGWGKSVDILGAEKLTMDVIVDEPTTVAIAAIPQSSKSGWANPERAVR 480

Qy  481 VNAEDFVQQTDGKYKAGLTITGEDAPNLKNIAFHEEDNNMNNIILFVGTDAADVIYLDNI 540
Db  481 VNAEDFVQQTDGKYKAGLTITGEDAPNLKNIAFHEEDNNMNNIILFVGTDAADVIYLDNI 540

Qy  541 KVIGTEVEIPVVHDPKGEAVLPSVFEDGTRQGWDWAGESGVKTALTIEEANGSNALSWEF 600
Db  541 KVIGTEVEIPVVHDPKGEAVLPSVFEDGTRQGWDWAGESGVKTALTIEEANGSNALSWEF 600

Qy  601 GYPEVKPSDNWATAPRLDFWKSDLVRGENDYVAFDFYLDPVRATEGAMNINLVFQPPTNG 660
Db  601 GYPEVKPSDNWATAPRLDFWKSDLVRGENDYVAFDFYLDPVRATEGAMNINLVFQPPTNG 660

Qy  661 YWVQAPKTYTINFDELEEANQVNGLYHYEVKINVRDITNIQDDTLLRNMMIIFADVESDF 720
Db  661 YWVQAPKTYTINFDELEEANQVNGLYHYEVKINVRDITNIQDDTLLRNMMIIFADVESDF 720

Qy  721 AGRVFVDNVRFEGAATTEPVEPEPVDPGEETPPVDEKEAKKEQKEAEKEEKEE 773
Db  721 AGRVFVDNVRFEGAATTEPVEPEPVDPGEETPPVDEKEAKKEQKEAEKEEKEE 773
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RESULT 2
US-11-044-363-2
; Sequence 2, Application US/11044363
; Publication No. US20050215450A1
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Schulein, Martin
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Gibson, Keith
; TITLE OF INVENTION: Endo-beta-1,4-glucanases
; FILE REFERENCE: 10184.204-US
; CURRENT APPLICATION NUMBER: US/11/044,363
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US/10/479,446
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-11-044-363-2

Query Match 100.0%; Score 4131; DB 6; Length 773;
Best Local Similarity 100.0%; Pred. No. 3.5e-298;
Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 AEGNTREDNFKHLLGNDNVKRPSEAGALQLQEVDGQMTLVDQHGEKIQLRGMSTHGLQWF 60
Db    1 AEGNTREDNFKHLLGNDNVKRPSEAGALQLQEVDGQMTLVDQHGEKIQLRGMSTHGLQWF 60

Qy   61 PEILNDNAYKALANDWESNMIRLAMYVGENGYASNPELIKSRVIKGIDLAIENDMYVIVD 120
Db   61 PEILNDNAYKALANDWESNMIRLAMYVGENGYASNPELIKSRVIKGIDLAIENDMYVIVD 120

Qy  121 WHVHAPGDPRDPVYAGAEDFFRDIAALYPNNPHIIYELANEPSSNNNGGAGIPNNEEGWN 180
Db  121 WHVHAPGDPRDPVYAGAEDFFRDIAALYPNNPHIIYELANEPSSNNNGGAGIPNNEEGWN 180

Qy  181 AVKEYADPIVEMLRDSGNADDNIIIVGSPNWSQRPDLAADNPINDHHTMYTVHFYTGSHA 240
Db  181 AVKEYADPIVEMLRDSGNADDNIIIVGSPNWSQRPDLAADNPINDHHTMYTVHFYTGSHA 240

Qy  241 ASTESYPPETPNSERGNVMSNTRYALENGVAVFATEWGTSQANGDGGPYFDEADVWIEFL 300
Db  241 ASTESYPPETPNSERGNVMSNTRYALENGVAVFATEWGTSQANGDGGPYFDEADVWIEFL 300

Qy  301 NENNISWANWSLTNKNEVSGAFTPFELGKSNATNLDPGPDHVWAPEELSLSGEYVRARIK 360
Db  301 NENNISWANWSLTNKNEVSGAFTPFELGKSNATNLDPGPDHVWAPEELSLSGEYVRARIK 360

Qy  361 GVNYEPIDRTKYTKVLWDFNDGTKQGFGVNSDSPNKELIAVDNENNTLKVSGLDVSNDVS 420
Db  361 GVNYEPIDRTKYTKVLWDFNDGTKQGFGVNSDSPNKELIAVDNENNTLKVSGLDVSNDVS 420

Qy  421 DGNFWANARLSADGWGKSVDILGAEKLTMDVIVDEPTTVAIAAIPQSSKSGWANPERAVR 480
Db  421 DGNFWANARLSADGWGKSVDILGAEKLTMDVIVDEPTTVAIAAIPQSSKSGWANPERAVR 480

Qy  481 VNAEDFVQQTDGKYKAGLTITGEDAPNLKNIAFHEEDNNMNNIILFVGTDAADVIYLDNI 540
Db  481 VNAEDFVQQTDGKYKAGLTITGEDAPNLKNIAFHEEDNNMNNIILFVGTDAADVIYLDNI 540
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Qy        541 KVIGTEVEIPVVHDPKGEAVLPSVFEDGTRQGWDWAGESGVKTALTIEEANGSNALSWEF 600
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Db        541 KVIGTEVEIPVVHDPKGEAVLPSVFEDGTRQGWDWAGESGVKTALTIEEANGSNALSWEF 600

Qy        601 GYPEVKPSDNWATAPRLDFWKSDLVRGENDYVAFDFYLDPVRATEGAMNINLVFQPPTNG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GYPEVKPSDNWATAPRLDFWKSDLVRGENDYVAFDFYLDPVRATEGAMNINLVFQPPTNG 660

Qy        661 YWVQAPKTYTINFDELEEANQVNGLYHYEVKINVRDITNIQDDTLLRNMMIIFADVESDF 720
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Db        661 YWVQAPKTYTINFDELEEANQVNGLYHYEVKINVRDITNIQDDTLLRNMMIIFADVESDF 720

Qy        721 AGRVFVDNVRFEGAATTEPVEPEPVDPGEETPPVDEKEAKKEQKEAEKEEKEE 773
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Db        721 AGRVFVDNVRFEGAATTEPVEPEPVDPGEETPPVDEKEAKKEQKEAEKEEKEE 773
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RESULT 3
US-10-383-630-2
; Sequence 2, Application US/10383630
; Publication No. US20040002431A1
; GENERAL INFORMATION:
; APPLICANT: HAKAMADA, YOSHIHIRO
; APPLICANT: SAWADA, KAZUHISA
; APPLICANT: ENDO, KEIJI
; APPLICANT: KODAMA, HIROSHI
; APPLICANT: WADA, YASUNAO
; APPLICANT: SHIKATA, SHITSU
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: Mutant alkali cellulase
; FILE REFERENCE: 234890US0
; CURRENT APPLICATION NUMBER: US/10/383,630
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: JP P2002-089531
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: JP P2003-013840
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Bacillus sp.KSM-S237
US-10-383-630-2

Query Match 98.3%; Score 4059; DB 4; Length 824;
Best Local Similarity 98.2%; Pred. No. 8.8e-293;
Matches 758; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 AEGNTREDNFKHLLGNDNVKRPSEAGALQLQEVDGQMTLVDQHGEKIQLRGMSTHGLQWF 60
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Db         30 AEGNTREDNFKHLLGNDNVKRPSEAGALQLQEVDGQMTLVDQHGEKIQLRGMSTHGLQWF 89

Qy         61 PEILNDNAYKALANDWESNMIRLAMYVGENGYASNPELIKSRVIKGIDLAIENDMYVIVD 120
              ||||||||||||:|||:|||||||||||||||:||||| ||| ||:||||||||||||
Db         90 PEILNDNAYKALSNDWDSNMIRLAMYVGENGYATNPELIKQRVIDGIELAIENDMYVIVD 149

Qy        121 WHVHAPGDPRDPVYAGAEDFFRDIAALYPNNPHIIYELANEPSSNNNGGAGIPNNEEGWN 180
              ||||||||||||||:||||:||||||||||||||||||||||||||||||||||||||||
Db        150 WHVHAPGDPRDPVYAGAKDFFREIAALYPNNPHIIYELANEPSSNNNGGAGIPNNEEGWK 209

Qy        181 AVKEYADPIVEMLRDSGNADDNIIIVGSPNWSQRPDLAADNPINDHHTMYTVHFYTGSHA 240
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Db        210 AVKEYADPIVEMLRKSGNADDNIIIVGSPNWSQRPDLAADNPIDDHHTMYTVHEYTGSHA 269

Qy        241 ASTESYPPETPNSERGNVMSNTRYALENGVAVFATEWGTSQANGDGGPYFDEADVWIEFL 300
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Db        270 ASTESYPSETPNSERGNVMSNTRYALENGVAVFATEWGTSQASGDGGPYFDEADVWIEFL 329

Qy        301 NENNISWANWSLTNKNEVSGAFTPFELGKSNATNLDPGPDHVWAPEELSLSGEYVRARIK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 NENNISWANWSLTNKNEVSGAFTPFELGKSNATNLDPGPDHVWAPEELSLSGEYVRARIK 389

Qy        361 GVNYEPIDRTKYTKVLWDFNDGTKQGFGVNSDSPNKELIAVDNENNTLKVSGLDVSNDVS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 GVNYEPIDRTKYTKVLWDFNDGTKQGFGVNSDSPNKELIAVDNENNTLKVSGLDVSNDVS 449

Qy        421 DGNFWANARLSADGWGKSVDILGAEKLTMDVIVDEPTTVAIAAIPQSSKSGWANPERAVR 480
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 DGNFWANARLSANGWGKSVDILGAEKLTMDVIVDEPTTVAIAAIPQSSKSGWANPERAVR 509

Qy        481 VNAEDFVQQTDGKYKAGLTITGEDAPNLKNIAFHEEDNNMNNIILFVGTDAADVIYLDNI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 VNAEDFVQQTDGKYKAGLTITGEDAPNLKNIAFHEEDNNMNNIILFVGTDAADVIYLDNI 569

Qy        541 KVIGTEVEIPVVHDPKGEAVLPSVFEDGTRQGWDWAGESGVKTALTIEEANGSNALSWEF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 KVIGTEVEIPVVHDPKGEAVLPSVFEDGTRQGWDWAGESGVKTALTIEEANGSNALSWEF 629

Qy        601 GYPEVKPSDNWATAPRLDFWKSDLVRGENDYVAFDFYLDPVRATEGAMNINLVFQPPTNG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 GYPEVKPSDNWATAPRLDFWKSDLVRGENDYVAFDFYLDPVRATEGAMNINLVFQPPTNG 689

Qy        661 YWVQAPKTYTINFDELEEANQVNGLYHYEVKINVRDITNIQDDTLLRNMMIIFADVESDF 720
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Db        690 YWVQAPKTYTINFDELEEANQVNGLYHYEVKINVRDITNIQDDTLLRNMMIIFADVESDF 749

Qy        721 AGRVFVDNVRFEGAATTEPVEPEPVDPGEETPPVDEKEAKKEQKEAEKEEKE 772
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Db        750 AGRVFVDNVRFEGAATTEPVEPEPVDPGEETPPVDEKEAKKEQKEAEKEEKE 801
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RESULT 4
US-10-479-214-2
; Sequence 2, Application US/10479214
; Publication No. US20040248279A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Sawada, Kazuhisa
; APPLICANT: Ozaki, Katsuya
; APPLICANT: Tohata, Masatoshi
; APPLICANT: Ozawa, Tadahiro
; APPLICANT: Endo, Keiji
; TITLE OF INVENTION: HOST MICROORGANISMS
; FILE REFERENCE: 244691US-0-PCT
; CURRENT APPLICATION NUMBER: US/10/479,214
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/JP02/05151
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: Japan 2001-160520
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-S237
US-10-479-214-2

Query Match 98.3%; Score 4059; DB 5; Length 824;
Best Local Similarity 98.2%; Pred. No. 8.8e-293;
Matches 758; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 AEGNTREDNFKHLLGNDNVKRPSEAGALQLQEVDGQMTLVDQHGEKIQLRGMSTHGLQWF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 AEGNTREDNFKHLLGNDNVKRPSEAGALQLQEVDGQMTLVDQHGEKIQLRGMSTHGLQWF 89

Qy         61 PEILNDNAYKALANDWESNMIRLAMYVGENGYASNPELIKSRVIKGIDLAIENDMYVIVD 120
              ||||||||||||:|||:|||||||||||||||:||||| ||| ||:||||||||||||
Db         90 PEILNDNAYKALSNDWDSNMIRLAMYVGENGYATNPELIKQRVIDGIELAIENDMYVIVD 149

Qy        121 WHVHAPGDPRDPVYAGAEDFFRDIAALYPNNPHIIYELANEPSSNNNGGAGIPNNEEGWN 180
              ||||||||||||||:||||:||||||||||||||||||||||||||||||||||||||||
Db        150 WHVHAPGDPRDPVYAGAKDFFREIAALYPNNPHIIYELANEPSSNNNGGAGIPNNEEGWK 209

Qy        181 AVKEYADPIVEMLRDSGNADDNIIIVGSPNWSQRPDLAADNPINDHHTMYTVHFYTGSHA 240
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